



PCT09

## RAW SEQUENCE LISTING

DATE: 05/07/2002

PATENT APPLICATION: US/09/926,169

TIME: 16:15:41

Input Set : A:\213993US0PCT.txt

Output Set: N:\CRF3\05072002\I926169.raw

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3 <110> APPLICANT: MARECHAL, ERIC
4     BLOCK, MARYSE
5     JOYARD, JACQUES
6     DOUCE, ROLAND
8 <120> TITLE OF INVENTION: SCREENING METHOD INVOLVING MGDG SYNTHASE
10 <130> FILE REFERENCE: 213993US0PCT
12 <140> CURRENT APPLICATION NUMBER: 09/926,169
C--> 13 <141> CURRENT FILING DATE: 2001-09-18
15 <150> PRIOR APPLICATION NUMBER: FR 99 03434
16 <151> PRIOR FILING DATE: 1999-03-19
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 23
24 <212> TYPE: DNA
25 <213> ORGANISM: Spinacia oleracea
27 <400> SEQUENCE: 1
28 ctcatgttgaa gggcagtagc acc
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 27
33 <212> TYPE: DNA
34 <213> ORGANISM: Spinacia oleracea
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40 <210> SEQ ID NO: 3
41 <211> LENGTH: 25
42 <212> TYPE: DNA
43 <213> ORGANISM: Spinacia oleracea
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50 <211> LENGTH: 26
51 <212> TYPE: DNA
52 <213> ORGANISM: Spinacia oleracea
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58 <210> SEQ ID NO: 5
59 <211> LENGTH: 28
60 <212> TYPE: DNA
61 <213> ORGANISM: Spinacia oleracea
63 <400> SEQUENCE: 5
64 gttctggatc ctcaagcagc acaagagt
67 <210> SEQ ID NO: 6

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68 <211> LENGTH: 28
69 <212> TYPE: DNA
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77 <211> LENGTH: 28
78 <212> TYPE: DNA
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81 <400> SEQUENCE: 7
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86 <211> LENGTH: 522
87 <212> TYPE: PRT
88 <213> ORGANISM: Spinacia oleracea
90 <400> SEQUENCE: 8
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93 1          5          10          15
96 Phe Val Pro Lys Leu Gly Asn Phe Val Leu Asn Ser Ser Leu His Gly
97          20          25          30
100 Asn Asn Ser Asn Gly Tyr Ser Ser Phe Ser Ser Asn Ser Val His Phe
101          35          40          45
104 Gly Gly Leu Ala Thr Gln Asn Arg Tyr Lys Phe Val Asn Ser Leu Ser
105          50          55          60
108 Phe Ser Lys Glu Gly Ser Asn Leu Lys Arg Ile Leu Ser Asp Phe Asn
109 65          70          75          80
112 Arg Val Ile Arg Leu His Cys Asp Arg Ile Pro Leu Gly Phe Ser Ser
113          85          90          95
116 Ile Gly Leu Asn Ser Gly Glu Ser Asn Gly Val Ser Asp Asn Gly His
117          100         105         110
120 Gly Val Leu Glu Asp Val Arg Val Pro Val Asn Ala Val Glu Pro Glu
121          115         120         125
124 Ser Pro Lys Arg Val Leu Ile Leu Met Ser Asp Thr Gly Gly Gly His
125          130         135         140
128 Arg Ala Ser Ala Glu Ala Ile Lys Ala Ala Phe Asn Glu Glu Phe Gly
129 145          150         155         160
132 Asp Asp Tyr Gln Val Phe Val Thr Asp Leu Trp Ser Glu His Thr Pro
133          165         170         175
136 Trp Pro Phe Asn Gln Leu Pro Arg Ser Tyr Asn Phe Leu Val Lys His
137          180         185         190
140 Gly Pro Leu Trp Lys Met Met Tyr Tyr Gly Thr Ser Pro Arg Val Ile
141          195         200         205
144 His Gln Ser Asn Phe Ala Ala Thr Ser Val Phe Ile Ala Arg Glu Val
145          210         215         220
148 Ala Arg Gly Leu Met Lys Tyr Gln Pro Asp Ile Ile Ile Ser Val His
149 225          230         235         240
152 Pro Leu Met Gln His Val Pro Leu Arg Ile Leu Arg Gly Arg Gly Leu
153          245         250         255
156 Leu Glu Lys Ile Val Phe Thr Thr Val Val Thr Asp Leu Ser Thr Cys

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157          260          265          270
160 His Pro Thr Trp Phe His Lys Leu Val Thr Arg Cys Tyr Cys Pro Ser
161          275          280          285
164 Asn Glu Val Ala Lys Arg Ala Thr Lys Ala Gly Leu Gln Pro Ser Gln
165          290          295          300
168 Ile Lys Val Tyr Gly Leu Pro Val Arg Pro Ser Phe Val Arg Ser Val
169 305          310          315          320
172 Arg Pro Lys Asn Glu Leu Arg Lys Glu Leu Gly Met Asp Glu His Leu
173          325          330          335
176 Pro Ala Val Leu Leu Met Gly Gly Gly Glu Gly Met Gly Pro Ile Glu
177          340          345          350
180 Ala Thr Ala Arg Ala Leu Gly Asn Ala Leu Tyr Asp Ala Asn Leu Gly
181          355          360          365
184 Glu Pro Thr Gly Gln Leu Leu Val Ile Cys Gly Arg Asn Lys Lys Leu
185          370          375          380
188 Ala Gly Lys Leu Ser Ser Ile Asp Trp Lys Ile Pro Val Gln Val Lys
189 385          390          395          400
192 Gly Phe Val Thr Lys Ile Glu Glu Cys Met Gly Ala Cys Asp Cys Ile
193          405          410          415
196 Ile Thr Lys Ala Gly Pro Gly Thr Ile Ala Glu Ala Met Ile Arg Gly
197          420          425          430
200 Leu Pro Ile Ile Leu Asn Asp Tyr Ile Ala Gly Gln Glu Ala Gly Asn
201          435          440          445
204 Val Pro Tyr Val Ile Glu Asn Gly Ile Gly Lys Tyr Leu Lys Ser Pro
205          450          455          460
208 Lys Glu Ile Ala Lys Thr Val Ser Gln Trp Phe Gly Pro Lys Ala Asn
209 465          470          475          480
212 Glu Leu Gln Ile Met Ser Gln Asn Ala Leu Lys His Ala Arg Pro Asp
213          485          490          495
216 Ala Val Phe Lys Ile Val His Asp Leu Asp Glu Leu Val Arg Gln Lys
217          500          505          510
220 Ile Phe Val Arg Gln Tyr Ser Cys Ala Ala
221          515          520
224 <210> SEQ ID NO: 9
225 <211> LENGTH: 525
226 <212> TYPE: PRT
227 <213> ORGANISM: Cucumis sativa
229 <400> SEQUENCE: 9
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232 1          5          10          15
235 Phe Ile Ser Gln Leu Gly Tyr Phe Ala Phe Ser Ser Arg Phe Leu Asn
236          20          25          30
239 Leu Asn Ser Glu Gly Cys Ser Gly Ser Ser Ser His Ser Leu Tyr Leu
240          35          40          45
243 Asn Gly Phe Glu Asn Tyr Arg Cys Val Lys Arg Pro Pro Arg Ser Gly
244          50          55          60
247 Ala Ser Leu Ser Leu Ser Ser Arg Gly Ser Ser Leu Arg Arg Phe
248 65          70          75          80
251 Val Asn Glu Phe Asn Asn Val Ile Lys Phe His Cys His Lys Pro Pro

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252				85				90				95				
255	Leu	Gly	Phe	Ala	Ser	Leu	Gly	Gly	Val	Ser	Asp	Glu	Thr	Asn	Gly	Ile
256				100				105				110				
259	Arg	Asp	Asp	Gly	Phe	Gly	Val	Ser	Gln	Asp	Gly	Ala	Leu	Pro	Leu	Asn
260			115					120				125				
263	Lys	Ile	Glu	Ala	Glu	Asn	Pro	Lys	Arg	Val	Leu	Ile	Leu	Met	Ser	Asp
264		130						135				140				
267	Thr	Gly	Gly	Gly	His	Arg	Ala	Ser	Ala	Glu	Ala	Ile	Lys	Ala	Ala	Phe
268	145					150					155				160	
271	Asn	Glu	Glu	Phe	Gly	Asn	Asn	Tyr	Gln	Val	Phe	Ile	Thr	Asp	Leu	Trp
272				165						170					175	
275	Thr	Asp	His	Thr	Pro	Trp	Pro	Phe	Asn	Gln	Leu	Pro	Arg	Ser	Tyr	Asn
276				180					185					190		
279	Phe	Leu	Val	Lys	His	Gly	Thr	Leu	Trp	Lys	Met	Thr	Tyr	Tyr	Val	Thr
280			195					200					205			
283	Ala	Pro	Lys	Val	Ile	His	Gln	Ser	Asn	Phe	Ala	Ala	Thr	Ser	Thr	Phe
284		210					215					220				
287	Ile	Ala	Arg	Glu	Val	Ala	Lys	Gly	Leu	Met	Lys	Tyr	Arg	Pro	Asp	Ile
288	225					230					235				240	
291	Ile	Ile	Ser	Val	His	Pro	Leu	Met	Gln	His	Val	Pro	Ile	Arg	Ile	Leu
292				245						250					255	
295	Arg	Ser	Lys	Gly	Leu	Leu	Asn	Lys	Ile	Val	Phe	Thr	Thr	Val	Val	Thr
296				260					265					270		
299	Asp	Leu	Ser	Thr	Cys	His	Pro	Thr	Trp	Phe	His	Lys	Leu	Val	Thr	Arg
300			275					280					285			
303	Cys	Tyr	Cys	Pro	Ser	Thr	Glu	Val	Ala	Lys	Arg	Ala	Leu	Thr	Ala	Gly
304		290					295					300				
307	Leu	Gln	Pro	Ser	Lys	Leu	Lys	Val	Phe	Gly	Leu	Pro	Val	Arg	Pro	Ser
308	305					310					315				320	
311	Phe	Val	Lys	Pro	Ile	Arg	Pro	Lys	Ile	Glu	Leu	Arg	Lys	Glu	Leu	Gly
312				325						330					335	
315	Met	Asp	Glu	Asn	Leu	Pro	Ala	Val	Leu	Leu	Met	Gly	Gly	Gly	Glu	Gly
316				340					345					350		
319	Met	Gly	Pro	Ile	Glu	Ala	Thr	Ala	Lys	Ala	Leu	Ser	Lys	Ala	Leu	Tyr
320			355					360					365			
323	Asp	Glu	Asn	His	Gly	Glu	Pro	Ile	Gly	Gln	Val	Leu	Val	Ile	Cys	Gly
324		370					375						380			
327	His	Asn	Lys	Lys	Leu	Ala	Gly	Arg	Leu	Arg	Ser	Ile	Asp	Trp	Lys	Val
328	385					390					395				400	
331	Pro	Val	Gln	Val	Lys	Gly	Phe	Val	Thr	Lys	Met	Glu	Glu	Cys	Met	Gly
332				405						410					415	
335	Ala	Cys	Asp	Cys	Ile	Ile	Thr	Lys	Ala	Gly	Pro	Gly	Thr	Ile	Ala	Glu
336				420					425					430		
339	Ala	Met	Ile	Arg	Gly	Leu	Pro	Ile	Ile	Leu	Asn	Asp	Tyr	Ile	Ala	Gly
340			435					440					445			
343	Gln	Glu	Ala	Gly	Asn	Val	Pro	Tyr	Val	Val	Glu	Asn	Gly	Cys	Gly	Lys
344		450					455					460				
347	Phe	Ser	Lys	Ser	Pro	Lys	Glu	Ile	Ala	Asn	Ile	Val	Ala	Lys	Trp	Phe
348	465					470					475				480	

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351 Gly Pro Lys Ala Asp Glu Leu Leu Ile Met Ser Gln Asn Ala Leu Arg
352                               485                               490                               495
355 Leu Ala Arg Pro Asp Ala Val Phe Lys Ile Val His Asp Leu His Glu
356                               500                               505                               510
359 Leu Val Lys Gln Arg Ser Phe Val Pro Gln Tyr Ser Gly
360                               515                               520                               525
363 <210> SEQ ID NO: 10
364 <211> LENGTH: 533
365 <212> TYPE: PRT
366 <213> ORGANISM: Arabidopsis thaliana
368 <400> SEQUENCE: 10
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374 Asp Phe Phe Pro Arg Leu Arg Gly Leu Thr Ser Arg Asn Arg Ser Pro
375                               20                               25                               30
378 Cys Ser Asn Ser Asp Gly Tyr Ala Leu Ser Ser Ser Asn Ala Leu Tyr
379                               35                               40                               45
382 Phe Asn Gly Phe Arg Thr Leu Pro Ser Arg Arg Met Gly Lys Thr Leu
383                               50                               55                               60
386 Ala Ser Leu Ser Phe Asn Thr Lys Ser Ser Ala Gly Ser Ser Leu Arg
387 65                               70                               75                               80
390 Arg Phe Ile Ser Asp Phe Asn Ser Phe Ile Arg Phe His Cys Asp Lys
391                               85                               90                               95
394 Val Val Pro Glu Ser Phe Ala Ser Val Gly Gly Val Gly Leu Ser Ser
395                               100                              105                              110
398 Asp Glu Asn Gly Ile Arg Glu Asn Gly Thr Gly Gly Val Leu Gly Glu
399                               115                              120                              125
402 Glu Gly Leu Pro Leu Asn Gly Val Glu Ala Asp Arg Pro Lys Lys Val
403                               130                              135                              140
406 Leu Ile Leu Met Ser Asp Thr Gly Gly Gly His Arg Ala Ser Ala Glu
407 145                              150                              155                              160
410 Ala Ile Arg Ala Ala Phe Asn Gln Glu Phe Gly Asp Glu Tyr Gln Val
411                               165                              170                              175
414 Phe Ile Thr Asp Leu Trp Thr Asp His Thr Pro Trp Pro Phe Asn Gln
415                               180                              185                              190
418 Leu Pro Arg Ser Tyr Asn Phe Leu Val Lys His Gly Thr Leu Trp Lys
419                               195                              200                              205
422 Met Thr Tyr Tyr Gly Thr Ser Pro Arg Ile Val His Gln Ser Asn Phe
423                               210                              215                              220
426 Ala Ala Thr Ser Thr Phe Ile Ala Arg Glu Ile Ala Gln Gly Leu Met
427 225                              230                              235                              240
430 Lys Tyr Gln Pro Asp Ile Ile Ile Ser Val His Pro Leu Met Gln His
431                               245                              250                              255
434 Val Pro Leu Arg Val Leu Arg Ser Lys Gly Leu Leu Lys Lys Ile Val
435                               260                              265                              270
438 Phe Thr Thr Val Ile Thr Asp Leu Ser Thr Cys His Pro Thr Trp Phe
439                               275                              280                              285
442 His Lys Leu Val Thr Arg Cys Tyr Cys Pro Ser Thr Glu Val Ala Lys
443                               290                              295                              300

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/926,169

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